

OIKE

## RAW SEQUENCE LISTING

DATE: 11/06/2001

PATENT APPLICATION: US/09/900,425

TIME: 12:06:37

Input Set : A:\isph522.txt

Output Set: N:\CRF3\11062001\I900425.raw

3 <110> APPLICANT: Wu, Hongjiang  
 4 Crooke, Stanley T.  
 6 <120> TITLE OF INVENTION: Human RNase III and Compositions and Uses Thereof  
 8 <130> FILE REFERENCE: ISPH-0522  
 W--> 9 <140> CURRENT APPLICATION NUMBER: US 09/900,425  
 10 <141> CURRENT FILING DATE: 2001-07-06  
 12 <150> PRIOR APPLICATION NUMBER: US 09/479,783  
 13 <151> PRIOR FILING DATE: 2000-01-07  
 15 <150> PRIOR APPLICATION NUMBER: US 08/870,608  
 16 <151> PRIOR FILING DATE: 1997-06-06  
 18 <150> PRIOR APPLICATION NUMBER: US 80/659,440  
 19 <151> PRIOR FILING DATE: 1996-06-06  
 21 <160> NUMBER OF SEQ ID NOS: 36  
 23 <170> SOFTWARE: PatentIn version 3.1

## ERRORED SEQUENCES

192 <210> SEQ ID NO: 2  
 193 <211> LENGTH: 1374  
 194 <212> TYPE: PRT  
 195 <213> ORGANISM: Homo sapiens  
 197 <400> SEQUENCE: 2  
 199 Met Met Gln Gly Asn Thr Cys His Arg Met Ser Phe His Pro Gly Arg  
 200 1 5 10 15  
 202 Gly Cys Pro Arg Gly Arg Gly Gly His Gly Ala Arg Pro Ser Ala Pro  
 203 20 25 30  
 205 Ser Phe Arg Pro Gln Asn Leu Arg Leu Leu His Pro Gln Gln Pro Pro  
 206 35 40 45  
 208 Val Gln Tyr Gln Tyr Glu Pro Pro Ser Ala Pro Ser Thr Thr Phe Ser  
 209 50 55 60  
 211 Asn Ser Pro Ala Pro Asn Phe Leu Pro Pro Arg Pro Asp Phe Val Pro  
 212 65 70 75 80  
 214 Phe Pro Pro Pro Met Pro Pro Ser Ala Gln Gly Pro Leu Pro Pro Cys  
 215 85 90 95  
 217 Pro Ile Arg Pro Pro Phe Pro Asn His Gln Met Arg His Pro Phe Pro  
 218 100 105 110  
 220 Val Pro Pro Cys Phe Pro Pro Met Pro Pro Met Pro Cys Pro Asn  
 221 115 120 125  
 223 Asn Pro Pro Val Pro Gly Ala Pro Pro Gly Gln Gly Thr Phe Pro Phe  
 224 130 135 140  
 226 Met Met Pro Pro Pro Ser Met Pro His Pro Pro Pro Pro Val Met  
 227 145 150 155 160  
 229 Pro Gln Gln Val Asn Tyr Gln Tyr Pro Pro Gly Tyr Ser His His Asn  
 230 165 170 175  
 232 Phe Pro Pro Pro Ser Phe Asn Ser Phe Gln Asn Asn Pro Ser Ser Phe  
 233 180 185 190

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```

235 Leu Pro Ser Ala Asn Asn Ser Ser Ser Pro His Phe Arg His Leu Pro
236      195      200      205
238 Pro Tyr Pro Leu Pro Lys Ala Pro Ser Glu Arg Arg Ser Pro Glu Arg
239      210      215      220
241 Leu Lys His Tyr Asp Asp His Arg His Arg Asp His Ser His Gly Arg
242 225      230      235      240
244 Gly Glu Arg His Arg Ser Leu Asp Arg Arg Glu Arg Gly Arg Ser Pro
245      245      250      255
247 Asp Arg Arg Arg Gln Asp Ser Arg Tyr Arg Ser Asp Tyr Asp Arg Gly
248      260      265      270
250 Arg Thr Pro Ser Arg His Arg Ser Tyr Glu Arg Ser Arg Glu Arg Glu
251      275      280      285
253 Arg Glu Arg His Arg His Arg Asp Asn Arg Arg Ser Pro Ser Leu Glu
254      290      295      300
256 Arg Ser Tyr Lys Lys Glu Tyr Lys Arg Ser Gly Arg Ser Tyr Gly Leu
257 305      310      315      320
259 Ser Val Val Pro Glu Pro Ala Gly Cys Thr Pro Glu Leu Pro Gly Glu
260      325      330      335
262 Ile Ile Lys Asn Thr Asp Ser Trp Ala Pro Pro Leu Glu Ile Val Asn
263      340      345      350
265 His Arg Ser Pro Ser Arg Glu Lys Lys Arg Ala Arg Trp Glu Glu Glu
266      355      360      365
268 Lys Asp Arg Trp Ser Asp Asn Gln Ser Ser Gly Lys Asp Lys Asn Tyr
269      370      375      380
271 Thr Ser Ile Lys Glu Lys Glu Pro Glu Glu Thr Met Pro Asp Lys Asn
272 385      390      395      400
274 Glu Glu Glu Glu Glu Glu Leu Leu Lys Pro Val Trp Ile Arg Cys Thr
275      405      410      415
277 His Ser Glu Asn Tyr Tyr Ser Ser Asp Pro Met Asp Gln Val Gly Asp
278      420      425      430
280 Ser Thr Val Val Gly Thr Ser Arg Glu Arg Asp Leu Tyr Asp Lys Phe
281      435      440      445
283 Glu Glu Glu Leu Gly Ser Arg Gln Glu Lys Ala Lys Ala Ala Arg Pro
284      450      455      460
286 Pro Trp Glu Pro Pro Lys Thr Lys Leu Asp Glu Asp Leu Glu Ser Ser
287 465      470      475      480
289 Ser Glu Ser Glu Cys Glu Ser Asp Glu Asp Ser Thr Cys Ser Ser Ser
290      485      490      495
292 Ser Asp Ser Glu Val Phe Asp Val Ile Ala Glu Ile Lys Arg Lys Lys
293      500      505      510
295 Ala His Pro Asp Arg Leu His Asp Glu Leu Trp Tyr Asn Asp Pro Gly
296      515      520      525
298 Gln Met Asn Asp Gly Pro Leu Cys Lys Cys Ser Ala Lys Ala Arg Arg
299      530      535      540
301 Thr Gly Ile Arg His Ser Ile Tyr Pro Gly Glu Glu Ala Ile Lys Pro
302 545      550      555      560
304 Cys Arg Pro Met Thr Asn Asn Ala Gly Arg Leu Phe His Tyr Arg Ile
305      565      570      575
307 Thr Val Ser Pro Pro Thr Asn Phe Leu Thr Asp Arg Pro Thr Val Ile

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```

308          580          585          590
310 Glu Tyr Asp Asp His Glu Tyr Ile Phe Glu Gly Phe Ser Met Phe Ala
311          595          600          605
313 His Ala Pro Leu Thr Asn Ile Pro Leu Cys Lys Val Ile Arg Phe Asn
314          610          615          620
316 Ile Asp Tyr Thr Ile His Phe Ile Glu Glu Met Met Pro Glu Asn Phe
317 625          630          635          640
319 Cys Val Lys Gly Leu Glu Leu Phe Ser Leu Phe Leu Phe Arg Asp Ile
320          645          650          655
322 Leu Glu Leu Tyr Asp Trp Asn Leu Lys Gly Pro Leu Phe Glu Asp Ser
323          660          665          670
325 Pro Pro Cys Cys Pro Arg Phe His Phe Met Pro Arg Phe Val Arg Phe
326          675          680          685
328 Leu Pro Asp Gly Gly Lys Glu Val Leu Ser Met His Gln Ile Leu Leu
329          690          695          700
331 Tyr Leu Leu Arg Cys Ser Lys Ala Leu Val Pro Glu Glu Ile Ala
332 705          710          715          720
334 Asn Met Leu Gln Trp Glu Glu Leu Glu Trp Gln Lys Tyr Ala Glu Glu
335          725          730          735
337 Cys Lys Gly Met Ile Val Thr Asn Pro Gly Thr Lys Pro Ser Ser Val
338          740          745          750
340 Arg Ile Asp Gln Leu Asp Arg Glu Gln Phe Asn Pro Asp Val Ile Thr
341          755          760          765
343 Phe Pro Ile Ile Val His Phe Gly Ile Arg Pro Ala Gln Leu Ser Tyr
344          770          775          780
346 Ala Gly Asp Pro Gln Tyr Gln Lys Leu Trp Lys Ser Tyr Val Lys Leu
347 785          790          795          800
349 Arg His Leu Leu Ala Asn Ser Pro Lys Val Lys Gln Thr Asp Lys Gln
350          805          810          815
352 Lys Leu Ala Gln Arg Glu Glu Ala Leu Gln Lys Ile Arg Gln Lys Asn
353          820          825          830
355 Thr Met Arg Arg Glu Val Thr Val Glu Leu Ser Ser Gln Gly Phe Trp
356          835          840          845
358 Lys Thr Gly Ile Arg Ser Asp Val Cys Gln His Ala Met Met Leu Pro
359          850          855          860
361 Val Leu Thr His His Ile Arg Tyr His Gln Cys Leu Met His Leu Asp
362 865          870          875          880
364 Lys Leu Ile Gly Tyr Thr Phe Gln Asp Arg Cys Leu Leu Gln Leu Ala
365          885          890          895
367 Met Thr His Pro Ser His His Leu Asn Phe Gly Met Asn Pro Asp His
368          900          905          910
370 Ala Arg Asn Ser Leu Ser Asn Cys Gly Ile Arg Gln Pro Lys Tyr Gly
371          915          920          925
373 Asp Arg Lys Val His His Met His Met Arg Lys Lys Gly Ile Asn Thr
374          930          935          940
376 Leu Ile Asn Ile Met Ser Arg Leu Gly Gln Asp Asp Pro Thr Pro Ser
377 945          950          955          960
379 Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Val
380          965          970          975

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```

382 Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe Pro Ser Leu Glu
383          980          985          990
385 Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val Gln Asn Gln His
386          995          1000          1005
388 Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Pro Phe Met Leu Tyr
389          1010          1015          1020
391 Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu Arg His Ala Met
392 1025          1030          1035          1040
394 Ala Asn Cys Phe Glu Ala Leu Ile Gly Ala Val Tyr Leu Glu Gly Ser
395          1045          1050          1055
397 Leu Glu Glu Ala Lys Gln Leu Phe Gly Arg Leu Leu Phe Asn Asp Pro
398          1060          1065          1070
400 Asp Leu Arg Glu Val Trp Leu Asn Tyr Pro Leu His Pro Leu Gln Leu
401          1075          1080          1085
403 Gln Glu Pro Asn Thr Asp Arg Gln Leu Ile Glu Thr Ser Pro Val Leu
404          1090          1095          1100
406 Gln Lys Leu Thr Glu Phe Glu Glu Ala Ile Gly Val Ile Phe Thr His
407 1105          1110          1115          1120
409 Val Arg Leu Leu Ala Arg Ala Phe Thr Leu Arg Thr Val Gly Phe Asn
410          1125          1130          1135
412 His Leu Thr Leu Gly His Asn Gln Arg Met Glu Phe Leu Gly Asp Ser
413          1140          1145          1150
415 Ile Met Gln Leu Val Ala Thr Glu Tyr Leu Phe Ile His Phe Pro Asp
416          1155          1160          1165
418 His His Glu Gly His Leu Thr Leu Leu Arg Ser Ser Leu Val Asn Asn
419          1170          1175          1180
421 Arg Thr Gln Ala Lys Val Ala Glu Glu Leu Gly Met Gln Glu Tyr Ala
422 1185          1190          1195          1200
424 Ile Thr Asn Asp Lys Thr Lys Arg Pro Val Gly Leu Arg Thr Lys Thr
425          1205          1210          1215
427 Leu Ala Asp Leu Leu Glu Ser Phe Ile Ala Ala Leu Tyr Thr Asp Lys
428          1220          1225          1230
430 Asp Leu Glu Tyr Val His Thr Phe Met Asn Val Cys Phe Phe Pro Arg
E--> 431          1235          1240          1245
433 Leu Lys Glu Phe Ile Leu Asn Gln Asp Trp Asn Asp Pro Lys Ser Gln
E--> 434 1250          1255          1260          1265
436 Leu Gln Gln Cys Cys Leu Thr Leu Arg Thr Glu Gly Lys Glu Pro Asp
E--> 437          1270          1275          1280
439 Ile Pro Leu Tyr Lys Thr Leu Gln Thr Val Gly Pro Ser His Ala Arg
E--> 440          1285          1290          1295
442 Thr Tyr Thr Val Ala Val Tyr Phe Lys Gly Glu Arg Ile Gly Cys Gly
E--> 443          1300          1305          1310
445 Lys Gly Pro Ser Ile Gln Gln Ala Glu Met Gly Ala Ala Met Asp Ala
E--> 446          1315          1320          1325
448 Leu Glu Lys Tyr Asn Phe Pro Gln Met Ala His Gln Lys Arg Phe Ile
E--> 449 1330          1335          1340          1345
451 Gly Arg Lys Tyr Arg Gln Glu Leu Lys Glu Met Arg Trp Glu Arg Glu
E--> 452          1350          1355          1360
455 His Gln Glu Arg Glu Pro Asp Glu Thr Glu Asp Ile Lys Lys

```

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Input Set : A:\isph522.txt

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E--> 456 1365 1370 *error align text*  
1095 <210> SEQ ID NO: 36  
1096 <211> LENGTH: 20  
1097 <212> TYPE: PRT  
1098 <213> ORGANISM: Homo sapiens  
1100 <400> SEQUENCE: 36  
1102 Cys Arg Trp Glu Arg Glu His Gln Glu Arg Glu Pro Asp Glu Thr Glu  
1103 1 5 10 15  
1105 Asp Ile Lys Lys  
1106 20  
E--> 1109 19  
E--> 1112 19  
E--> 1115 1  
E--> 1118 2 *delete text*

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/900,425

DATE: 11/06/2001

TIME: 12:06:38

Input Set : A:\isph522.txt

Output Set: N:\CRF3\11062001\I900425.raw

L:9 M:283 W: Missing Blank Line separator, <140> field identifier  
L:431 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
M:332 Repeated in SeqNo=2  
L:787 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:788 M:283 W: Missing Blank Line separator, <220> field identifier  
L:798 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
L:799 M:283 W: Missing Blank Line separator, <220> field identifier  
L:809 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
L:810 M:283 W: Missing Blank Line separator, <220> field identifier  
L:820 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11  
L:821 M:283 W: Missing Blank Line separator, <220> field identifier  
L:831 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
L:832 M:283 W: Missing Blank Line separator, <220> field identifier  
L:842 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13  
L:843 M:283 W: Missing Blank Line separator, <220> field identifier  
L:853 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14  
L:854 M:283 W: Missing Blank Line separator, <220> field identifier  
L:864 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15  
L:865 M:283 W: Missing Blank Line separator, <220> field identifier  
L:875 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16  
L:876 M:283 W: Missing Blank Line separator, <220> field identifier  
L:885 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17  
L:897 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18  
L:898 M:283 W: Missing Blank Line separator, <220> field identifier  
L:908 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19  
L:909 M:283 W: Missing Blank Line separator, <220> field identifier  
L:919 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20  
L:920 M:283 W: Missing Blank Line separator, <220> field identifier  
L:930 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21  
L:931 M:283 W: Missing Blank Line separator, <220> field identifier  
L:941 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22  
L:942 M:283 W: Missing Blank Line separator, <220> field identifier  
L:952 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23  
L:953 M:283 W: Missing Blank Line separator, <220> field identifier  
L:963 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24  
L:964 M:283 W: Missing Blank Line separator, <220> field identifier  
L:974 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25  
L:975 M:283 W: Missing Blank Line separator, <220> field identifier  
L:985 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26  
L:986 M:283 W: Missing Blank Line separator, <220> field identifier  
L:996 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27  
L:997 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1007 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28  
L:1008 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1018 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29  
L:1019 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1029 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30  
L:1030 M:283 W: Missing Blank Line separator, <220> field identifier

**VERIFICATION SUMMARY**

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Input Set : A:\isph522.txt

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L:1040 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31  
L:1041 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1051 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32  
L:1052 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1062 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33  
L:1063 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1073 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34  
L:1074 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1109 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36  
M:332 Repeated in SeqNo=36

**STATISTICS SUMMARY**

PATENT APPLICATION: US/09/900,425

DATE: 11/06/2001

TIME: 12:06:38

Input Set : A:\isph522.txt

Output Set: N:\CRF3\11062001\I900425.raw

Application Serial Number: US/09/900,425

Alpha or Numeric: Numeric

Application Class:

Application File Date: 07-06-2001

Art Unit: OIPE

Software Application: PatentIn

Total Number of Sequences: 36

Total Nucleotides: 5531

Total Amino Acids: 2900

Number of Errors: 13

Number of Warnings: 27

Number of Corrections: 27

**MESSAGE SUMMARY**

220 C: 27 (Keyword misspelled or invalid format)

283 W: 27 (Missing Blank Line separator)

332 E: 13 ((32) Invalid/Missing Amino Acid Numbering)